GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 14:56:34 ; Search time 413.564 Seconds
(without alignments)
10776.324 Million cell updates/sec

Title: US-09-625-573-3
Perfect score: 1979
Sequence: 1 CAGGACTGCCTGAGACAAGC.....ATATGCAATATAAAATTTAG 1979

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1977.4	99.9	1979	16	AAQ96298	Human monocyte che
2	1943.8	98.2	143068	21	AAF21105	Human low adenosin
3	1943.8	98.2	143068	21	AAF21272	Human low adenosin
4	1943.8	98.2	143068	21	AAA34983	Human adenosine re
5	1943.8	98.2	143068	21	AAA35150	Human adenosine re
6	1943.8	98.2	143068	24	ABL68124	Ovary cancer relat
7	1943.8	98.2	149412	21	AAA35151	Human adenosine re
8	1943.8	98.2	152740	21	AAF21273	Human low adenosin
9	1313	66.3	10528	24	ABL32334	Human immune syste
c 10	1286.4	65.0	10528	24	ABL32335	Human immune syste
11	1083	54.7	1083	22	AAS12140	Human wild-type CC
12	1081.4	54.6	1083	22	AAS12139	Human CCR2-64I pol
13	1079.8	54.6	1083	23	ABI97976	Non-endogenous hum
14	1078.2	54.5	1083	18	AAT96976	Human monocyte che
15	980	49.5	2232	16	AAQ96297	Human monocyte che
16	704.6	35.6	1059	18	AAT85163	Macaque chemokine
17	703.4	35.5	1225	19	AAT76920	DNA encoding human
18	703.4	35.5	1225	24	ABA02317	Human CC chemokine
19	703.4	35.5	1376	22	AAH26903	Human HIV-1 co-rec
20	703.4	35.5	1477	18	AAT90117	cDNA for human CCR
21	703.4	35.5	1477	22	AAF87099	Human CCR5 cDNA se
22	703.4	35.5	3383	18	AAT85161	Human chemokine re
23	703.4	35.5	3383	21	AAF21271	Human low adenosin
24	703.4	35.5	3383	21	AAA35149	Human adenosine re
25	703.4	35.5	3383	22	AAD08577	Human chemokine re
26	703.4	35.5	9141	24	ABA97318	Human chemokine (C
27	702	35.5	1376	20	AAV84126	HIV-1 co-receptor
28	701.8	35.5	1225	24	ABA02318	Human CCR5 Gln 55
29	701.8	35.5	1414	22	AAF26390	Human HDGNR10 cDNA
30	701.4	35.4	1059	22	AAI65463	Nucleotide sequenc
31	700.2	35.4	1414	18	AAT44042	Human G-protein ch
32	700.2	35.4	1414	21	AAZ91481	Human G-protein ch
33	700.2	35.4	1414	22	AAD13181	Human G-protein ch
34	700.2	35.4	1414	22	AAD13282	Human G-protein ch
35	700.2	35.4	1414	24	ABK51853	DNA encoding human
36	700	35.4	1059	19	AAV23992	Human CC-CKR5 codi
37	700	35.4	1059	24	ABA97319	Human chemokine (C
38	700	35.4	1071	20	AAV84125	HIV-1 co-receptor
39	699.2	35.3	5674	20	AAZ24738	Human chemokine re
40	697.6	35.3	1056	22	AAD13198	Human G-protein ch
41	697.6	35.3	1056	22	AAD13299	Human G-protein ch
42	697.6	35.3	1056	24	ABK51870	DNA encoding human
43	696.8	35.2	1059	23	ABI97978	Non-endogenous hum
44	692.2	35.0	1255	19	AAT76919	DNA encoding human
45	683.4	34.5	1344	20	AAV84159	HIV-1 co-receptor

ALIGNMENTS

RESULT 1
AAQ96298
ID AAQ96298 standard; cDNA; 1979 BP.
XX
AC AAQ96298;
XX
DT 29-DEC-1995 (first entry)
XX
DE Human monocyte chemoattractant protein-1 receptor MCP-1RB.
XX
KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 81..1160
FT /*tag= a
XX
PN WO9519436-A.
XX
PD 20-JUL-1995.
XX
PF 11-JAN-1995; 95WO-US00476.
XX
PR 13-JAN-1994; 94US-0182962.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Charo I, Coughlin S;
XX
DR WPI; 1995-263866/34.
DR P-PSDB; AAR79166.

XX
PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
PT for identifying antagonists and for treating diseases characterised by
PT monocytic infiltrates
XX
PS Disclosure; Fig 2; 84pp; English.
XX
CC To identify and clone new members of the chemokine receptor gene
CC family, degenerate oligo primers were designed corresp. to the
CC conserved sequences R79167 in the second and R79168 in the third
CC transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8
CC receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293.
CC The degenerate oligo incorporating EcoRI and XhoI sites at their 5'
CC ends are Q96299 and Q96300. Amplification of cDNA derived from MM6
CC cells with the primers yieled a number of PCR products. One cDNA
CC appeared to encode a novel protein. To obtain a full-length version
CC of this clone, a MM6 cDNA library was constructed in pFROG and probed
CC with the PCR product. A 2.1 kb cDNA clone was obtd. Analysis of
CC additional clones in the MM6 cDNA library revealed a second
CC sequence that was identical to the 2.1 kb cDNA sequence first obtd.
CC from the 5' UTR through the putative seventh transmembrane domain
CC but contained a different cytoplasmic tail. The second sequence
CC appears to represent alternative splicing of the carboxyl-terminal
CC tail of the MCP-1R protein. The two sequences are denoted MCP-1RA
CC and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature
CC MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB
CC has a mol. wt. of about 41,000 daltons.
XX
SQ Sequence 1979 BP; 530 A; 434 C; 452 G; 563 T; 0 other;

Query Match 99.9%; Score 1977.4; DB 16; Length 1979;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 CAGGACTGCCTGAGACAAGCCACAAGCTGAACAGAGAAAGTGGATTGAACAAGGACGCAT 60
Db       1 CAGGACTGCCTGAGACAAGCCACAAGCTGAACAGAGAAAGTGGATTGAACAAGGACGCAT 60

Qy      61 TTCCCCAGTACATCCACAACATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCA 120
Db      61 TTCCCCAGTACATCCACAACATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCA 120

Qy     121 ACGAGAGCGGTGAAGAAGTCACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATA 180
Db     121 ACGAGAGCGGTGAAGAAGTCACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATA 180

Qy     181 AATTTGACGTGAAGCAAATTGGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCA 240
Db     181 AATTTGACGTGAAGCAAATTGGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCA 240

Qy     241 TCTTTGGTTTTGTGGGCAACATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGA 300
Db     241 TCTTTGGTTTTGTGGGCAACATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGA 300

Qy     301 AGTGCTTGACTGACATTTACCTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTA 360
Db     301 AGTGCTTGACTGACATTTACCTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTA 360

Qy     361 CTCTCCCATTGTGGGCTCACTCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCA 420
Db     361 CTCTCCCATTGTGGGCTCACTCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCA 420

Qy     421 AATTATTCACAGGGCTGTATCACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCC 480
Db     421 AATTATTCACAGGGCTGTATCACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCC 480

Qy     481 TGACAATCGATAGATACCTGGCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGG 540
Db     481 TGACAATCGATAGATACCTGGCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGG 540

Qy     541 TCACCTTTGGGGTGGTGACAAGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCC 600
Db     541 TCACCTTTGGGGTGGTGACAAGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCC 600

Qy     601 CAGGAATCATCTTTACTAAATGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATT 660
Db     601 CAGGAATCATCTTTACTAAATGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATT 660

Qy     661 TTCCACGAGGATGGAATAATTTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGC 720
Db     661 TTCCACGAGGATGGAATAATTTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGC 720

Qy     721 CGCTGCTCATCATGGTCATCTGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAA 780
Db     721 CGCTGCTCATCATGGTCATCTGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAA 780

Qy     781 ACGAGAAGAAGAGGCATAGGGCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTC 840
Db     781 ACGAGAAGAAGAGGCATAGGGCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTC 840

Qy     841 TCTTCTGGACTCCCTATAACATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCC 900
Db     841 TCTTCTGGACTCCCTATAACATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCC 900

Qy     901 TGAGTAACTGTGAAAGCACCAGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTG 960
Db     901 TGAGTAACTGTGAAAGCACCAGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTG 960

Qy     961 GGATGACTCACTGCTGCATCAATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAA 1020
Db     961 GGATGACTCACTGCTGCATCAATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAA 1020

Qy    1021 GGTATCTCTCGGTGTTCTTCCGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAG 1080
Db    1021 GGTATCTCTCGGTGTTCTTCCGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAG 1080

Qy    1081 TTTTCTACAGGGAGACAGTGGATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGC 1140
Db    1081 TTTTCTACAGGGAGACAGTGGATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGC 1140

Qy    1141 AGGAAGTCTCGGCTGGTTTATAAAACGAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGA 1200
Db    1141 AGGAAGTCTCGGCTGGTTTATAAAACGAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGA 1200

Qy    1201 TAACAATCTGTATATAACAACAAACTTCAAGGGTTTGTTGAACAATAGAAACCTGTAAAG 1260
Db    1201 TAACAATCTGTATATAACAACAAACTTCAAGGGTTTGTTGAACAATAGAAACCTGTAAAG 1260

Qy    1261 CAGGTGCCCAGGAACCTCAGGGCTGTGTGTACTAATACAGACTATGTCACCCAATGCATA 1320
Db    1261 CAGGTGCCCAGGAACCTCAGGGCTGTGTGTACTAATACAGACTATGTCACCCAATGCATA 1320

Qy    1321 TCCAACATGTGCTCAGGGAATAATCCAGAAAAACTGTGGGTAGAGACTTTGACTCTCCAG 1380
Db    1321 TCCAACATGTGCTCAGGGAATAATCCAGAAAAACTGTGGGTAGAGACTTTGACTCTCCAG 1380

Qy    1381 AAAGCTCATCTCAGCTCCTGAAAAATGCCTCATTACCTTGTGCTAATCCTCTTTTTCTAG 1440
Db    1381 AAAGCTCATCTCAGCTCCTGAAAAATGCCTCATTACCTTGTGCTAATCCTCTTTTTCTAG 1440

Qy    1441 TCTTCATAATTTCTTCACTCAATCTCTGATTCTGTCAATGTCTTGAAATCAAGGGCCAGC 1500
Db    1441 TCTTCATAATTTCTTCACTCAATCTCTGATTCTGTCAATGTCTTGAAATGAAGGGCCAGC 1500

Qy    1501 TGGAGGTGAAGAAGAGAATGTGACAGGCACAGATGAATGGGAGTGAGGGATAGTGGGGTC 1560
Db    1501 TGGAGGTGAAGAAGAGAATGTGACAGGCACAGATGAATGGGAGTGAGGGATAGTGGGGTC 1560

Qy    1561 AGGGCTGAGAGGAGAAGGAGGGAGACATGAGCATGGCTGAGCCTGGACAAAGACAAAGGT 1620
Db    1561 AGGGCTGAGAGGAGAAGGAGGGAGACATGAGCATGGCTGAGCCTGGACAAAGACAAAGGT 1620

Qy    1621 GAGCAAAGGGCTCACGCATTCAGCCAGGAGATGATACTGGTCCTTAGCCCCATCTGCCAC 1680
Db    1621 GAGCAAAGGGCTCACGCATTCAGCCAGGAGATGATACTGGTCCTTAGCCCCATCTGCCAC 1680
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Qy   1681 GTGTATTTAACCTTGAAGGGTTCACCAGGTCAGGGAGAGTTTGGGAACTGCAATAACCTG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GTGTATTTAACCTTGAAGGGTTCACCAGGTCAGGGAGAGTTTGGGAACTGCAATAACCTG 1740

Qy   1741 GGAGTTTTGGTGGAGTCCGATGATTCTCTTTTGCATAAGTGCATGACATATTTTTGCTTT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGAGTTTTGGTGGAGTCCGATGATTCTCTTTTGCATAAGTGCATGACATATTTTTGCTTT 1800

Qy   1801 ATTACAGTTTATCTATGGCACCCATGCACCTTACATTTGAAATCTATGAAATATCATGCT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATTACAGTTTATCTATGGCACCCATGCACCTTACATTTGAAATCTATGAAATATCATGCT 1860

Qy   1861 CCATTGTTCAGATGCTTCTTAGGCCACATCCCCCTGTCTAAAAAATTCAGAAAATTTTTGT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CCATTGTTCAGATGCTTCTTAGGCCACATCCCCCTGTCTAAAAAATTCAGAAAATTTTTGT 1920

Qy   1921 TTATAAAAGATGCATTATCTATGATATGCTAATATATGTATATGCAATATAAAATTTAG 1979
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TTATAAAAGATGCATTATCTATGATATGCTAATATATGTATATGCAATATAAAATTTAG 1979
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RESULT 2
AAF21105
ID AAF21105 standard; DNA; 143068 BP.
XX
AC AAF21105;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2672.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 924-957; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 143068 BP; 41194 A; 30122 C; 32403 G; 39349 T; 0 other;

Query Match 98.2%; Score 1943.8; DB 21; Length 143068;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy     27 CTGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 86
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46052 CAGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 46111

Qy     87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46112 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 46171

Qy    147 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46172 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 46231

Qy    207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46232 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 46291

Qy    267 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46292 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 46351

Qy    327 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46352 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 46411

Qy    387 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46412 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 46471

Qy    447 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46472 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 46531

Qy    507 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46532 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 46591

Qy    567 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46592 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 46651

Qy    627 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46652 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 46711

Qy    687 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 746
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Db  46712 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 46771

Qy    747 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 806

Db  46772 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 46831

Qy    807 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 866

Db  46832 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 46891

Qy    867 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 926

Db  46892 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 46951

Qy    927 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 986

Db  46952 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 47011

Qy    987 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 1046

Db  47012 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 47071

Qy   1047 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 1106

Db  47072 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 47131

Qy   1107 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 1166

Db  47132 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 47191

Qy   1167 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 1226

Db  47192 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 47251

Qy   1227 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 1286

Db  47252 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 47311

Qy   1287 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 1346

Db  47312 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 47371

Qy   1347 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 1406

Db  47372 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 47431

Qy   1407 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 1466

Db  47432 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 47491

Qy   1467 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 1526

Db  47492 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 47551

Qy   1527 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 1586

Db  47552 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 47611

Qy   1587 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 1646

Db  47612 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 47671

Qy   1647 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 1706

Db  47672 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 47731

Qy   1707 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 1766

Db  47732 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 47791

Qy   1767 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 1826

Db  47792 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 47851

Qy   1827 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 1886

Db  47852 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 47911

Qy   1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946

Db  47912 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 47971

Qy   1947 TGCTAATATATGTATATGCAATATAAA 1973

Db  47972 TGCTAATATATGTATATGCAATATATA 47998
```

RESULT 3
AAF21272
ID AAF21272 standard; DNA; 143068 BP.
XX
AC AAF21272;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2839.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 1186-1219; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system

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CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 143068 BP; 41194 A; 30122 C; 32403 G; 39349 T; 0 other;

  Query Match             98.2%;  Score 1943.8;  DB 21;  Length 143068;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1945;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      27 CTGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 86
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46052 CAGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 46111

Qy      87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46112 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 46171

Qy     147 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46172 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 46231

Qy     207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46232 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 46291

Qy     267 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46292 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 46351

Qy     327 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46352 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 46411

Qy     387 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46412 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 46471

Qy     447 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46472 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 46531

Qy     507 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46532 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 46591

Qy     567 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46592 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 46651

Qy     627 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46652 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 46711

Qy     687 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46712 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 46771

Qy     747 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46772 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 46831

Qy     807 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46832 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 46891

Qy     867 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46892 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 46951

Qy     927 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46952 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 47011

Qy     987 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 1046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47012 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 47071

Qy    1047 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47072 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 47131

Qy    1107 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 1166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47132 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 47191

Qy    1167 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 1226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47192 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 47251

Qy    1227 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 1286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47252 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 47311

Qy    1287 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 1346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47312 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 47371

Qy    1347 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 1406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47372 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 47431

Qy    1407 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 1466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47432 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 47491

Qy    1467 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 1526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47492 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 47551

Qy    1527 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 1586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47552 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 47611

Qy    1587 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 1646
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47612 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 47671

Qy    1647 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 1706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47672 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 47731

Qy    1707 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 1766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47732 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 47791

Qy    1767 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 1826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47792 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 47851

Qy    1827 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 1886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47852 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 47911
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Qy   1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47912 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 47971

Qy   1947 TGCTAATATATGTATATGCAATATAAA 1973
          ||||||||||||||||||||||||| |
Db  47972 TGCTAATATATGTATATGCAATATATA 47998


RESULT 4
AAA34983
ID   AAA34983 standard; DNA; 143068 BP.
XX
AC   AAA34983;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2672.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 851-882; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 143068 BP; 41194 A; 30122 C; 32402 G; 39350 T; 0 other;

  Query Match             98.2%;  Score 1943.8;  DB 21;  Length 143068;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1945;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     27 CTGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 86
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46052 CAGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 46111

Qy     87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46112 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 46171

Qy    147 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46172 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 46231

Qy    207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46232 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 46291

Qy    267 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46292 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 46351

Qy    327 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46352 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 46411

Qy    387 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46412 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 46471

Qy    447 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46472 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 46531

Qy    507 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46532 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 46591

Qy    567 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46592 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 46651

Qy    627 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46652 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 46711

Qy    687 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46712 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 46771

Qy    747 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46772 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 46831

Qy    807 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46832 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 46891

Qy    867 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46892 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 46951

Qy    927 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46952 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 47011
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Qy    987 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 1046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47012 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 47071

Qy   1047 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 1106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47072 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 47131

Qy   1107 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 1166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47132 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 47191

Qy   1167 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 1226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47192 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 47251

Qy   1227 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 1286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47252 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 47311

Qy   1287 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 1346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47312 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 47371

Qy   1347 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 1406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47372 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 47431

Qy   1407 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 1466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47432 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 47491

Qy   1467 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 1526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47492 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 47551

Qy   1527 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 1586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47552 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 47611

Qy   1587 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 1646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47612 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 47671

Qy   1647 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 1706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47672 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 47731

Qy   1707 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47732 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 47791

Qy   1767 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47792 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 47851

Qy   1827 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47852 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 47911

Qy   1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47912 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 47971

Qy   1947 TGCTAATATATGTATATGCAATATAAA 1973
          ||||||||||||||||||||||||| |
Db  47972 TGCTAATATATGTATATGCAATATATA 47998


RESULT 5
AAA35150
ID   AAA35150 standard; DNA; 143068 BP.
XX
AC   AAA35150;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:24.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 1106-1138; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 143068 BP; 41194 A; 30126 C; 32402 G; 39346 T; 0 other;

  Query Match             98.2%;  Score 1943.8;  DB 21;  Length 143068;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1945;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      27 CTGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 86
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db  46052 CAGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 46111

Qy     87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46112 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 46171

Qy    147 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46172 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 46231

Qy    207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46232 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 46291

Qy    267 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46292 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 46351

Qy    327 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46352 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 46411

Qy    387 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46412 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 46471

Qy    447 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46472 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 46531

Qy    507 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46532 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 46591

Qy    567 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46592 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 46651

Qy    627 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46652 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 46711

Qy    687 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46712 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 46771

Qy    747 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46772 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 46831

Qy    807 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46832 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 46891

Qy    867 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46892 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 46951

Qy    927 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46952 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 47011

Qy    987 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 1046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47012 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 47071

Qy   1047 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 1106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47072 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 47131

Qy   1107 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 1166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47132 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 47191

Qy   1167 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 1226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47192 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 47251

Qy   1227 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 1286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47252 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 47311

Qy   1287 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 1346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47312 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 47371

Qy   1347 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 1406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47372 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 47431

Qy   1407 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 1466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47432 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 47491

Qy   1467 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 1526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47492 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 47551

Qy   1527 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 1586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47552 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 47611

Qy   1587 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 1646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47612 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 47671

Qy   1647 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 1706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47672 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 47731

Qy   1707 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47732 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 47791

Qy   1767 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47792 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 47851

Qy   1827 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47852 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 47911

Qy   1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47912 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 47971

Qy   1947 TGCTAATATATGTATATGCAATATAAA 1973
          |||||||||||||||||||||||||
Db  47972 TGCTAATATATGTATATGCAATATATA 47998
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RESULT 6
ABL68124
ID   ABL68124 standard; DNA; 143068 BP.
XX
AC   ABL68124;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Ovary cancer related gene sequence SEQ ID NO:6461.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
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OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1; SEQ ID 6461; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 143068 BP; 41194 A; 30122 C; 32403 G; 39349 T; 0 other;

Query Match 98.2%; Score 1943.8; DB 24; Length 143068;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      27 CTGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 86
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46052 CAGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 46111

Qy      87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46112 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 46171

Qy     147 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46172 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 46231

Qy     207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46232 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 46291

Qy     267 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46292 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 46351

Qy     327 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46352 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 46411

Qy     387 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46412 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 46471

Qy     447 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46472 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 46531

Qy     507 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46532 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 46591

Qy     567 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46592 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 46651

Qy     627 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46652 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 46711

Qy     687 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46712 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 46771

Qy     747 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46772 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 46831

Qy     807 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46832 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 46891

Qy     867 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  46892 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 46951

Qy    927 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46952 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 47011

Qy    987 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 1046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47012 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 47071

Qy   1047 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 1106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47072 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 47131

Qy   1107 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 1166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47132 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 47191

Qy   1167 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 1226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47192 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 47251

Qy   1227 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 1286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47252 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 47311

Qy   1287 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 1346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47312 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 47371

Qy   1347 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 1406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47372 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 47431

Qy   1407 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 1466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47432 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 47491

Qy   1467 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 1526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47492 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 47551

Qy   1527 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 1586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47552 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 47611

Qy   1587 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 1646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47612 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 47671

Qy   1647 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 1706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47672 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 47731

Qy   1707 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47732 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 47791

Qy   1767 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47792 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 47851

Qy   1827 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47852 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 47911

Qy   1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  47912 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 47971

Qy   1947 TGCTAATATATGTATATGCAATATAAA 1973
          |||||||||||||||||||||||||
Db  47972 TGCTAATATATGTATATGCAATATATA 47998
```

RESULT 7
AAA35151
ID AAA35151 standard; DNA; 149412 BP.
XX
AC AAA35151;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:25.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1138-1171; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 149412 BP; 43049 A; 31388 C; 33852 G; 41123 T; 0 other;

Query Match 98.2%; Score 1943.8; DB 21; Length 149412;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      27 CTGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 86
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52396 CAGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 52455

Qy      87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52456 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 52515

Qy     147 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52516 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 52575

Qy     207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52576 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 52635

Qy     267 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52636 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 52695

Qy     327 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52696 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 52755

Qy     387 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52756 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 52815

Qy     447 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52816 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 52875

Qy     507 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52876 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 52935

Qy     567 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52936 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 52995

Qy     627 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52996 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 53055

Qy     687 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53056 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 53115

Qy     747 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53116 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 53175

Qy     807 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53176 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 53235

Qy     867 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53236 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 53295

Qy     927 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53296 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 53355

Qy     987 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 1046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53356 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 53415

Qy    1047 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53416 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 53475

Qy    1107 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 1166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53476 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 53535

Qy    1167 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 1226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53536 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 53595

Qy    1227 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 1286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53596 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 53655

Qy    1287 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 1346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53656 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 53715

Qy    1347 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 1406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53716 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 53775

Qy    1407 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 1466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53776 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 53835

Qy    1467 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 1526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53836 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 53895

Qy    1527 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 1586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53896 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 53955

Qy    1587 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 1646
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53956 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 54015

Qy    1647 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 1706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   54016 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 54075

Qy    1707 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 1766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   54076 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 54135

Qy    1767 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 1826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   54136 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 54195

Qy    1827 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 1886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   54196 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 54255

Qy    1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   54256 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 54315

Qy    1947 TGCTAATATATGTATATGCAATATAAA 1973
           |||||||||||||||||||||||||  |
Db   54316 TGCTAATATATGTATATGCAATATATA 54342
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RESULT 8
AAF21273
ID AAF21273 standard; DNA; 152740 BP.
XX
AC AAF21273;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2840.
XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 1219-1254; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 152740 BP; 44169 A; 32023 C; 34549 G; 41999 T; 0 other;

Query Match 98.2%; Score 1943.8; DB 21; Length 152740;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      27 CTGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 86
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52396 CAGAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTG 52455

Qy      87 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52456 TCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACC 52515

Qy     147 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52516 TTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCC 52575

Qy     207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52576 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 52635

Qy     267 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52636 GTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 52695

Qy     327 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52696 AACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCT 52755

Qy     387 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52756 GCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATC 52815

Qy     447 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52816 GGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 52875

Qy     507 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52876 GTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTG 52935

Qy     567 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52936 ATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAG 52995

Qy     627 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52996 AAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCAC 53055

Qy     687 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53056 ACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTAC 53115

Qy     747 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53116 TCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTG 53175

Qy     807 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53176 AGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTC 53235

Qy     867 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53236 ATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAA 53295

Qy     927 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53296 CTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCC 53355

Qy     987 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 1046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53356 ATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAG 53415

Qy    1047 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53416 CACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGA 53475

Qy    1107 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 1166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   53476 GTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAAC 53535
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Qy   1167 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 1226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53536 GAGGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACT 53595

Qy   1227 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 1286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53596 TCAAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGT 53655

Qy   1287 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 1346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53656 GTGTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCC 53715

Qy   1347 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 1406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53716 AGAAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAAT 53775

Qy   1407 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 1466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53776 GCCTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTC 53835

Qy   1467 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 1526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53836 TGATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAG 53895

Qy   1527 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 1586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53896 GCACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGAC 53955

Qy   1587 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 1646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  53956 ATGAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCA 54015

Qy   1647 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 1706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  54016 GGAGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACC 54075

Qy   1707 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  54076 AGGTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTC 54135

Qy   1767 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  54136 TCTTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATG 54195

Qy   1827 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  54196 CACCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCA 54255

Qy   1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  54256 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 54315

Qy   1947 TGCTAATATATGTATATGCAATATAAA 1973
          |||||||||||||||||||||||||
Db  54316 TGCTAATATATGTATATGCAATATATA 54342
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RESULT 9
ABL32334
ID ABL32334 standard; DNA; 10528 BP.
XX
AC ABL32334;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 307.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 307; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 10528 BP; 3072 A; 86 C; 2419 G; 4951 T; 0 other;

Query Match 66.3%; Score 1313; DB 24; Length 10528;
Best Local Similarity 79.7%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 395; Indels 0; Gaps 0;

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Qy     29 GAACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTGTC 88
          ||| |||||||||||||||| |||||||| ||||    |||| ||  |.|| ||| |||
Db   8327 GAATAGAGAAAGTGGATTGAATAAGGACGTATTTTTTTAGTATATTTATAATATGTTGTT 8386

Qy     89 CACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACCTT 148
          | || ||||| |||||||||| |||||||  |||||||||||||||||||| |  |  ||
Db   8387 TATATTTCGTTTTCGGTTTATTAGAAATATTAACGAGAGCGGTGAAGAAGTTATTATTTT 8446

Qy    149 TTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCA 208
          |||||||||||||||||||| |   ||| |||||||||||||||| |||||||||   |
Db   8447 TTTTGATTATGATTACGGTGTTTTTTGTTATAAATTTGACGTGAAGTAAATTGGGGTTTA 8506

Qy    209 ACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGT 268
          | |  ||  | || | || ||| ||||||| || |||||||||||||| || ||| ||||
Db   8507 ATTTTTGTTTTCGTTTTATTCGTTGGTGTTTATTTTTGGTTTTGTGGGTAATATGTTGGT 8566

Qy    269 CGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAA 328
          |||  | || |||||||| || |||||| ||||||| |||| ||| |||||  || | ||
Db   8567 CGTTTTTATTTTAATAAATTGTAAAAAGTTGAAGTGTTTGATTGATATTTATTTGTTTAA 8626

Qy    329 CCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGC 388
            |||  || | |||| || ||||| |||||| | |   |||||||| | | | || ||
Db   8627 TTTGGTTATTTTTGATTTGTTTTTTTTTATTATTTTTTTATTGTGGGTTTATTTTGTTGT 8686

Qy    389 AAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGG 448
          |||||||||||| |||||||||| |||||| |||||||| | |||| ||||| | |||||
Db   8687 AAATGAGTGGGTTTTTGGGAATGTAATGTGTAAATTATTTATAGGGTTGTATTATATCGG 8746

Qy    449 TTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGT 508
          |||||||||||||| || || || ||  | ||| ||||||||||||  ||| ||||||
Db   8747 TTATTTTGGCGGAATTTTTTTTATTATTTTTTTGATAATCGATAGATATTTGGTTATTGT 8806
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Qy    509 CCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGAT 568
Db   8807 TTATGTTGTGTTTGTTTTAAAAGTTAGGACGGTTATTTTTGGGGTGGTGATAAGTGTGAT 8866

Qy    569 CACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAA 628
Db   8867 TATTTGGTTGGTGGTTGTGTTTGTTTTTGTTTTAGGAATTATTTTTATTAAATGTTAGAA 8926

Qy    629 AGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCACAC 688
Db   8927 AGAAGATTTTGTTTATGTTTGTGGTTTTTATTTTTTACGAGGATGGAATAATTTTTATAT 8986

Qy    689 AATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTACTC 748
Db   8987 AATAATGAGGAATATTTTGGGGTTGGTTTTGTCGTTGTTTATTATGGTTATTTGTTATTC 9046

Qy    749 GGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTGAG 808
Db   9047 GGGAATTTTGAAAATTTGTTTCGGTGTCGAAACGAGAAGAAGAGGTATAGGGTAGTGAG 9106

Qy    809 AGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTCAT 868
Db   9107 AGTTATTTTTATTATTATGATTGTTTATTTTTTTTTTTGGATTTTTTATAATATTGTTAT 9166

Qy    869 TCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAACT 928
Db   9167 TTTTTTGAATATTTTTTAGGAATTTTTCGGTTTGAGTAATTGTGAAAGTATTAGTTAATT 9226

Qy    929 GGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCCAT 988
Db   9227 GGATTAAGTTACGTAGGTGATAGAGATTTTTGGGATGATTTATTGTTGTATTAATTTTAT 9286

Qy    989 CATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAGCA 1048
Db   9287 TATTTATGTTTTCGTTGGGGAGAAGTTTAGAAGGTATTTTTCGGTGTTTTTTCGAAAGTA 9346

Qy   1049 CATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGAGT 1108
Db   9347 TATTATTAAGCGTTTTTGTAAATAATGTTTAGTTTTTTATAGGGAGATAGTGGATGGAGT 9406

Qy   1109 GACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAACGA 1168
Db   9407 GATTTTAATAAATACGTTTTTTATTGGGGAGTAGGAAGTTTCGGTTGGTTTATAAAACGA 9466

Qy   1169 GGAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACTTC 1228
Db   9467 GGAGTAGTTTGATTGTTGTTTATAAAGGGAGATAATAATTTGTATATAATAATAAATTTT 9526

Qy   1229 AAGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGTGT 1288
Db   9527 AAGGGTTTGTTGAATAATAGAAATTTGTAAAGTAGGTGTTTAGGAATTTTAGGGTTGTGT 9586

Qy   1289 GTACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCCAG 1348
Db   9587 GTATTAATATAGATTATGTTATTTAATGTATATTTAATATGTGTTTAGGGAATAATTTAG 9646

Qy   1349 AAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAATGC 1408
Db   9647 AAAAATTGTGGGTAGAGATTTTGATTTTTTAGAAAGTTTATTTTAGTTTTTGAAAAATGT 9706

Qy   1409 CTCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTCTG 1468
Db   9707 TTTATTATTTTGTGTTAATTTTTTTTTTTTAGTTTTTATAATTTTTTTATTTAATTTTTG 9766

Qy   1469 ATTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAGGC 1528
Db   9767 ATTTTGTTAATGTTTTGAAATTAAGGGTTAGTTGGAGGTGAAGAAGAGAATGTGATAGGT 9826

Qy   1529 ACAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGACAT 1588
Db   9827 ATAGATGAATGGGAGTGAGGGATAGTGGGGTTAGGGTTGAGAGGAGAAGGAGGGAGATAT 9886.

Qy   1589 GAGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCAGG 1648

                                                                        |||
Db   9887 GAGTATGGTTGAGTTTGGATAAAGATAAAGGTGAGTAAAGGGTTTACGTATTTAGTTAGG 9946

Qy   1649 AGATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACCAG 1708
Db   9947 AGATGATATTGGTTTTTAGTTTTATTTGTTACGTGTATTTAATTTTGAAGGGTTTATTAG 10006

Qy.  1709 GTCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTCTC 1768
Db  10007 GTTAGGGAGAGTTTGGGAATTGTAATAATTTGGGAGTTTTGGTGGAGTTCGATGATTTTT 10066

Qy   1769 TTTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATGCA 1828
Db  10067 TTTTGTATAAGTGTATGATATATTTTTGTTTTATTATAGTTTATTTATGGTATTTATGTA 10126

Qy   1829 CCTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCACA 1888
Db  10127 TTTTATATTTGAAATTTATGAAATATTATGTTTTATTGTTTAGATGTTTTTTAGGTTATA 10186

Qy   1889 TCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATATG 1948
Db  10187 TTTTTTTGTTTAAAAATTTAGAAAATTTTTGTTTATAAAAGATGTATTATTTATGATATG 10246

Qy   1949 CTAATATATGTATATGCAATATAAA 1973
Db  10247 TTAATATATGTATATGTAATATATA 10271
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RESULT 10
ABL32335/c
ID ABL32335 standard; DNA; 10528 BP.
XX
AC ABL32335;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 308.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 308; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,

CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 10528 BP; 2873 A; 86 C; 2164 G; 5405 T; 0 other;

Query Match 65.0%; Score 1286.4; DB 24; Length 10528;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 411; Indels 0; Gaps 0;

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Qy      30 AACAGAGAAAGTGGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTGTCC 89
           |||| | ||| |  ||| |||||  |||||||||||||| ||||||||||||||| || |||
Db    2201 AACAAAAAAAATAAATTAAACAAAAACGCATTTCCCCAATACATCCACAACATACTATCC 2142

Qy      90 ACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACCTTT 149
           |||||||||||||| ||||||| |||||||||||| | || | || || ||||||||||
Db    2141 ACATCTCGTTCTCGATTTATCAAAAATACCAACGAAAACGATAAAAAAATCACCACCTTT 2082

Qy     150 TTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAA 209
           ||| ||||| |||||| | |||||| |||||||||| |||| || ||||||    |||||
Db    2081 TTTAATTATAATTACGATACTCCCTATCATAAATTTAACGTAAAACAAATTAAAACCCAA 2022

Qy     210 CTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTC 269
           ||||| |||||||||||||||  | |||||||||  |||| |   |||||| ||  ||
Db    2021 CTCCTACCTCCGCTCTACTCGCTAATATTCATCTTTAATTTTATAAACAACATACTAATC 1962

Qy     270 GTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAAC 329
           |||||||||||||||||| |||||| || || | ||| ||| |||||||||| ||||||
Db    1961 GTCCTCATCTTAATAAACTACAAAAAACTAAAATACTTAACTAACATTTACCTACTCAAC 1902

Qy     330 CTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCA 389
           ||  |||||||| |||| |||||||||||||||||||||| |   |||||||| || ||
Db    1901 CTAACCATCTCTAATCTACTTTTTCTTATTACTCTCCCATTATAAACTCACTCTACTACA 1842

Qy     390 AATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGT 449
           ||| | |   |||||   ||| |||| | ||||||||||||   || ||||||||| |
Db    1841 AATAAATAAATCTTTAAAAATACAATATACAAATTATTCACAAAACTATATCACATCGAT 1782

Qy     450 TATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTC 509
           ||||||  || ||||||||||||||||||| |||||||||| ||||||  ||||| ||
Db    1781 TATTTTAACGAAATCTTCTTCATCATCCTCCTAACAATCGATAAATACCTAACTATTATC 1722

Qy     510 CATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATC 569
           ||| || | ||| |||||||| |||  ||| ||||||||    | | |||| | | |||
Db    1721 CATACTATATTTACTTTAAAAACCAAAACGATCACCTTTAAAATAATAACAAATATAATC 1662

Qy     570 ACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAA 629
           ||||  ||  |  || | ||| ||||| |||||  |||||||||||||||| ||| |||
Db    1661 ACCTAATTAATAACTATATTTACTTCTATCCCAAAAATCATCTTTACTAAATACCAAAAA 1602

Qy     630 GAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCACACA 689
           || ||||| ||||| ||| |  |||||||||||||||  ||  ||||||||||||||||
Db    1601 AAAAATTCTATTTATATCTATAACCCTTATTTTCCACGAAAATAAAATAATTTCCACACA 1542

Qy     690 ATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTACTCG 749
           |||||  |  |||||||||    ||  |||| |||||  |||||||| |||||| |||||||
Db    1541 ATAATAAAAAACATTTTAAAACTAATCCTACCGCTACTCATCATAATCATCTACTACTCG 1482

Qy     750 GGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTGAGA 809
           ||||||  |||||||| |||||  |||||||||  ||  ||  |  ||||   ||  | | |
Db    1481 AAAATCCTAAAAACCCTACTTCGATATCGAAACGAAAAAAAAAAACATAAAACAATAAAA 1422

Qy     810 GTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTCATT 869
           |||||||||||||||| ||| ||||||||||||||  |||||||||||||||  |||||
Db    1421 ATCATCTTCACCATCATAATTATTTACTTTCTCTTCTAAACTCCCTATAACATTATCATT 1362

Qy     870 CTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAACTG 929
           |||||  ||||||||||  |||||||| ||| | |||||  | |||  |||||  ||||||
Db    1361 CTCCTAAACACCTTCCAAAAATTCTTCGACCTAAATAACTATAAAAACACCAATCAACTA 1302

Qy     930 GACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATC 989
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           ||||| |||||||  | ||| | ||||||   || |||||||| || ||||||||||||
Db    1301 AACCAAACCACGCAAATAACAAAAACTCTTAAAATAACTCACTACTACATCAATCCCATC 1242

Qy     990 ATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAGCAC 1049
           |||||| ||||||||     | || |||| ||  |||||||| | ||||||||||| |||
Db    1241 ATCTATACCTTCGTTAAAAAAAAATTCAAAAAATATCTCTCGATATTCTTCCGAAAACAC 1182

Qy    1050 ATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGGATGGAGTG 1109
           |||||||| ||||||| |||||||| |||| |||||||||   | ||| |  ||  | |
Db    1181 ATCACCAAACGCTTCTACAAACAATATCCAATTTTCTACAAAAAAACAATAAATAAAATA 1122

Qy    1110 ACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTATAAAACGAG 1169
           |||||||||||||||||||||||||    | ||  || ||||| ||  ||||||||||||
Db    1121 ACTTCAACAAACACGCCTTCCACTAAAAAACAAAAAATCTCGACTAATTTATAAAACGAA 1062

Qy    1170 GAGCAGTTTGATTGTTGTTTATAAAGGGAGATAACAATCTGTATATAACAACAAACTTCA 1229
           | || ||| ||| || |||||||||   | ||||||||||  ||||||||||||||||||||
Db    1061 AAACAATTTAATTATTATTTATAAAAAAAAATAACAATCTATATATAACAACAAACTTCA 1002

Qy    1230 AGGGTTTGTTGAACAATAGAAACCTGTAAAGCAGGTGCCCAGGAACCTCAGGGCTGTGTG 1289
           |   ||| || ||||||| |||||| |||| ||  | ||||  |||||||   || | |
Db    1001 AAAATTTATTAAACAATAAAAACCTATAAAACAAATACCCAAAAACCTCAAAACTATATA 942

Qy    1290 TACTAATACAGACTATGTCACCCAATGCATATCCAACATGTGCTCAGGGAATAATCCAGA 1349
           |||||||||| ||||| ||||||||| |||||||||||| | ||||   |||||||| |
Db     941 TACTAATACAAACTATATCACCCAATACATATCCAACATATACTCAAAAAATAATCCAAA 882

Qy    1350 AAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAATGCC 1409
           |||||| |   || | ||||| |||||||| ||| |||||||| ||||| |||||| ||
Db     881 AAAACTATAAATAAAAACTTTAACTCTCCAAAAAACTCATCTCAACTCCTAAAAAATACC 822

Qy    1410 TCATTACCTTGTGCTAATCCTCTTTTTCTAGTCTTCATAATTTCTTCACTCAATCTCTGA 1469
           |||||||||| | |||||||||||||||| |||||||||||||||||||||||||||| |
Db     821 TCATTACCTTATACTAATCCTCTTTTTCTAATCTTCATAATTTCTTCACTCAATCTCTAA 762

Qy    1470 TTCTGTCAATGTCTTGAAATCAAGGGCCAGCTGGAGGTGAAGAAGAGAATGTGACAGGCA 1529
           |||| ||||| |||| |||||||   ||| ||  |  | || || | ||| | |||  ||
Db     761 TTCTATCAATATCTTAAAATCAAAAACCAACTAAAAATAAAAAAAAAAAATATAACAAACA 702

Qy    1530 CAGATGAATGGGAGTGAGGGATAGTGGGGTCAGGGCTGAGAGGAGAAGGAGGGAGACATG 1589
           || || |||   | | |   ||| |   ||  | | |  | ||   |  | ||||
Db     701 CAAATAAATAAAAATAAAAAATAATAAATCAAAACTAAAAAAAAAAAAAAAAAAACATA 642

Qy    1590 AGCATGGCTGAGCCTGGACAAAGACAAAGGTGAGCAAAGGGCTCACGCATTCAGCCAGGA 1649
           | |||  || | |||  ||||| |||||  | | ||||  |||||||||||| |||  |
Db     641 AACATAACTAAACCTAAACAAAAACAAAAATAAACAAAAAACTCACGCATTCAACCAAAA 582

Qy    1650 GATGATACTGGTCCTTAGCCCCATCTGCCACGTGTATTTAACCTTGAAGGGTTCACCAGG 1709
           || |||||  |||||| |||||||| |||||| |||||||||| ||   |||||||
Db     581 AATAATACTAATCCTTAACCCCATCTACCACGTATATTTAACCTTAAAAAATTCACCAAA 522

Qy    1710 TCAGGGAGAGTTTGGGAACTGCAATAACCTGGGAGTTTTGGTGGAGTCCGATGATTCTCT 1769
           |||   | | |||   |||| |||||||||   | ||||  |  | |||||| |||||||
Db     521 TCAAAAAAAATTTAAAAACTACAATAACCTAAAAATTTTAATAAAATCCGATAATTCTCT 462

Qy    1770 TTTGCATAAGTGCATGACATATTTTTGCTTTATTACAGTTTATCTATGGCACCCATGCAC 1829
           |||  ||||| | ||| |||||||||| |||||||||  |||||||||  ||||||| |||
Db     461 TTTACATAAATACATAACATATTTTTACTTTATTACAATTTATCTATAACACCCATACAC 402

Qy    1830 CTTACATTTGAAATCTATGAAATATCATGCTCCATTGTTCAGATGCTTCTTAGGCCACAT 1889
           |||||||||  |||||||| |||||||| |||||||  |||| || |||||||  ||||||
Db     401 CTTACATTTAAAATCTATAAAATATCATACTCCATTATTCAAATACTTCTTAAACCACAT 342

Qy    1890 CCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATATGC 1949
           |||||| |||||||||||  |||||||| |||||||| || |||||||||  |||| |
Db     341 CCCCCTATCTAAAAATTCAAAAAATTTTTATTTATAAAAAATACATTATCTATAATATAC 282

Qy    1950 TAATATATGTATATGCAATATAAA 1973
           |||||||| ||||| ||||||| |
Db     281 TAATATATATATATACAATATATA 258

RESULT 11
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AAS12140
ID   AAS12140 standard; DNA; 1083 BP.
XX
AC   AAS12140;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Human wild-type CCR2-64V polynucleotide.
XX
KW   Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;
KW   single nucleotide polymorphism; hypercholesterolaemia; ds.
XX
OS   Homo sapiens.
XX
PN   WO200162796-A1.
XX
PD   30-AUG-2001.
XX
PF   22-FEB-2001; 2001WO-GB00755.
XX
PR   22-FEB-2000; 2000GB-0004183.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Valdes AM,  Groot PHE,  Spurr NK;
XX
DR   WPI; 2001-550086/61.
DR   P-PSDB; AAU07614.
XX
PT   Diagnosing atherosclerosis or susceptibility to atherosclerosis in a
PT   subject, by determining a single nucleotide polymorphism in specific
PT   codon of a polynucleotide encoding human CCR2 receptor in genome of the
PT   subject -
XX
PS   Claim 3; Page 20-21; 28pp; English.
XX
CC   The invention relates to diagnosing atherosclerosis (or susceptibility
CC   to) in a subject by determining expression or activity of the human
CC   CCR2-64I polypeptide (a polymorphic variant form of the human CCR2
CC   receptor) or the CCR2-64V polypeptide (human CCR2 receptor), by screening
CC   for a single nucleotide polymorphism in codon 64 of the polynucleotide
CC   encoding the CCR2 receptor. This results in production of CCR2-64I,
CC   whereby polymorphic variants are associated with a lower incidence of
CC   atherosclerosis. The presence or amount of CCR2-64I/V in a sample can
CC   also be analysed. The sequences of the invention can be used for
CC   predicting the response of a patient to drug treatment, for predicting
CC   the disease outcome in a patient and also for the production of a
CC   treatment for hypercholesterolaemia. The sequence represents DNA encoding
CC   the wild-type receptor polypeptide CCR2-64V.
XX
SQ   Sequence 1083 BP; 255 A; 260 C; 247 G; 321 T; 0 other;

  Query Match             54.7%;  Score 1083;  DB 22;  Length 1083;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-304;
  Matches 1083;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      81 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 60

Qy     141 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 120

Qy     201 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 180

Qy     261 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 240

Qy     321 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 300

Qy     381 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 360

Qy     441 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 420

Qy     501 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 480

Qy     561 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 540

Qy     621 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 600

Qy     681 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 660

Qy     741 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 720

Qy     801 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 780

Qy     861 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 840

Qy     921 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 900

Qy     981 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 960

Qy    1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1020

Qy    1101 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1080

Qy    1161 TAA 1163
           |||
Db    1081 TAA 1083


RESULT 12
AAS12139
ID   AAS12139 standard; DNA; 1083 BP.
XX
AC   AAS12139;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Human CCR2-64I polymorphic variant polynucleotide.
XX
KW   Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;
KW   single nucleotide polymorphism; hypercholesterolaemia; ds.
XX
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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(190,G)
FT                   /*tag= a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200162796-A1.
XX
PD   30-AUG-2001.
XX
PF   22-FEB-2001; 2001WO-GB00755.
XX
PR   22-FEB-2000; 2000GB-0004183.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Valdes AM,  Groot PHE,  Spurr NK;
XX
DR   WPI; 2001-550086/61.
DR   P-PSDB; AAU07613.
XX
PT   Diagnosing atherosclerosis or susceptibility to atherosclerosis in a
PT   subject, by determining a single nucleotide polymorphism in specific
PT   codon of a polynucleotide encoding human CCR2 receptor in genome of the
PT   subject -
XX
PS   Claim 3; Page 20; 28pp; English.
XX
CC   The invention relates to diagnosing atherosclerosis (or susceptibility
CC   to) in a subject by determining expression or activity of the human
CC   CCR2-64I polypeptide (a polymorphic variant form of the human CCR2
CC   receptor) or the CCR2-64V polypeptide (human CCR2 receptor), by screening
CC   for a single nucleotide polymorphism in codon 64 of the polynucleotide
CC   encoding the CCR2 receptor. This results in production of CCR2-64I,
CC   whereby polymorphic variants are associated with a lower incidence of
CC   atherosclerosis. The presence or amount of CCR2-64I/V in a sample can
CC   also be analysed. The sequences of the invention can be used for
CC   predicting the response of a patient to drug treatment, for predicting
CC   the disease outcome in a patient and also for the production of a
CC   treatment for hypercholesterolaemia. The sequence represents DNA encoding
CC   the polymorphic variant polypeptide CCR2-64I.
XX
SQ   Sequence 1083 BP; 256 A; 260 C; 246 G; 321 T; 0 other;

  Query Match           54.6%;  Score 1081.4;  DB 22;  Length 1083;
  Best Local Similarity 99.9%;  Pred. No. 2.8e-303;
  Matches 1082;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      81 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 60

Qy     141 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 120

Qy     201 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 180

Qy     261 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 320
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATGCTGGTCATCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 240

Qy     321 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 300

Qy     381 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 360

Qy     441 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 420

Qy     501 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 480

Qy     561 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 540

Qy     621 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 600

Qy     681 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 660

Qy     741 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 720

Qy     801 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 780

Qy     861 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 840

Qy     921 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 900

Qy     981 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 960

Qy    1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1020

Qy    1101 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1080

Qy    1161 TAA 1163
           |||
Db    1081 TAA 1083


RESULT 13
ABI97976
ID   ABI97976 standard; cDNA; 1083 BP.
XX
AC   ABI97976;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Non-endogenous human GPCR cDNA, SEQ ID NO: 472.
XX
KW   Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW   constitutively activated GPCR; agonist; disease; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177172-A2.
XX
PD   18-OCT-2001.
XX
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PF   05-APR-2001; 2001WO-US11098.
XX
PR   07-APR-2000; 2000US-195747P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Lehmann-Bruinsma K,  Liaw CW,  Lin I;
XX
DR   WPI; 2001-648759/74.
DR   P-PSDB; ABB56340.
XX
PT   Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT   disease treatment, comprises contacting candidate compounds with
PT   versions of GPCRs -
XX
PS   Example 2; Page 273-274; 394pp; English.
XX
CC   The invention relates to G protein-coupled receptors (GPCRs) for which
CC   the endogenous ligand has been identified. Non-endogenous
CC   constitutively activated versions of known GPCRs are used in the
CC   invention for the direct identification of candidate compounds as
CC   receptor agonists, inverse agonists or partial agonists. Such
CC   agonists are useful as therapeutic agents for diseases or disorders
CC   associated with GPCRs. The present sequence encodes a non-endogenous
CC   version of a known human GPCR.
XX
SQ   Sequence 1083 BP; 257 A; 260 C; 246 G; 320 T; 0 other;

  Query Match             54.6%;  Score 1079.8;  DB 23;  Length 1083;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-303;
  Matches 1081;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      81 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 60

Qy     141 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 120

Qy     201 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 180

Qy     261 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 240

Qy     321 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 300

Qy     381 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 360

Qy     441 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 420

Qy     501 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 480

Qy     561 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 540

Qy     621 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 600

Qy     681 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 660

Qy     741 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 720

Qy     801 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 860
           |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GCAAAGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 780

Qy     861 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 840

Qy     921 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 900

Qy     981 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 960

Qy    1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1020

Qy    1101 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1080

Qy    1161 TAA 1163
           |||
Db    1081 TAA 1083


RESULT 14
AAT96976
ID   AAT96976 standard; cDNA; 1083 BP.
XX
AC   AAT96976;
XX
DT   27-FEB-1998  (first entry)
XX
DE   Human monocyte chemoattractant protein 1 receptor encoding cDNA.
XX
KW   Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;
KW   inflammatory disease; viral; allergy; diabetes; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1083
FT                   /*tag=  a
FT                   /product= Monocyte_chemoattractant_protein_1_receptor
XX
PN   JP09238688-A.
XX
PD   16-SEP-1997.
XX
PF   11-MAR-1996;   96JP-0053574.
XX
PR   11-MAR-1996;   96JP-0053574.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
DR   WPI; 1997-506557/47.
DR   P-PSDB; AAW35833.
XX
PT   DNA encoding human monocyte chemoattractant protein 1 receptor -
PT   used to treat tumours and inflammatory, viral, infectious, allergic,
PT   diabetic and central nervous system diseases
XX
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PS   Claim 1; Page 12; 15pp; Japanese.
XX
CC   The present sequence encodes human monocyte chemoattractant protein 1
CC   (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA
CC   are used for the prevention and treatment of tumours and inflammatory,
CC   viral, infectious, allergic, diabetic and central nervous system
CC   diseases.
XX
SQ   Sequence 1083 BP; 257 A; 259 C; 245 G; 322 T; 0 other;

  Query Match             54.5%;  Score 1078.2;  DB 18;  Length 1083;
  Best Local Similarity   99.7%;  Pred. No. 2.4e-302;
  Matches 1080;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      81 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 60

Qy     141 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 120

Qy     201 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 260
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     121 GGGGCCCAACTCCTGCCTCCACTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 180

Qy     261 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 240

Qy     321 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 300

Qy     381 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 360

Qy     441 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 420

Qy     501 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 480

Qy     561 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 540

Qy     621 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 600

Qy     681 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 660

Qy     741 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 720

Qy     801 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAT 780

Qy     861 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 840

Qy     921 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 900

Qy     981 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 960

Qy    1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1020

Qy    1101 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1160
           ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    1021 GATGGAGTGACTTCAACAAACACACCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1080

Qy    1161 TAA 1163
           |||
Db    1081 TAA 1083


RESULT 15
AAQ96297
ID   AAQ96297 standard; cDNA; 2232 BP.
XX
AC   AAQ96297;
XX
DT   29-DEC-1995  (first entry)
XX
DE   Human monocyte chemoattractant protein-1 receptor MCP-1RA.
XX
KW   Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             40..1161
FT                   /*tag=  a
XX
PN   WO9519436-A.
XX
PD   20-JUL-1995.
XX
PF   11-JAN-1995;   95WO-US00476.
XX
PR   13-JAN-1994;   94US-0182962.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Charo I,  Coughlin S;
XX
DR   WPI; 1995-263866/34.
DR   P-PSDB; AAR79165.
XX
PT   DNA encoding monocyte chemo-attractant protein-1 receptor  - used partic.
PT   for identifying antagonists and for treating diseases characterised by
PT   monocytic infiltrates
XX
PS   Disclosure; Fig 1; 84pp; English.
XX
CC   To identify and clone new members of the chemokine receptor gene
CC   family, degenerate oligo primers were designed corresp. to the
CC   conserved sequences R79167 in the second and R79168 in the third
CC   transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8
CC   receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293.
CC    The degenerate oligo incorporating EcoRI and XhoI sites at their 5'
CC   ends are Q96299 and Q96300. Amplification of cDNA derived from MM6
CC   cells with the primers yieled a number of PCR products. One cDNA
CC   appeared to encode a novel protein. To obtain a full-length version
CC   of this clone, a MM6 cDNA library was constructed in pFROG and probed
CC   with the PCR product. A 2.1 kb cDNA clone was obtd. Analysis of
CC   additional clones in the MM6 cDNA library revealed a second
CC   sequence that was identical to the 2.1 kb cDNA sequence first obtd.
CC   from the 5' UTR through the putative seventh transmembrane domain
CC   but contained a different cytoplasmic tail. The second sequence
CC   appears to represent alternative splicing of the carboxyl-terminal
```

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CC   tail of the MCP-1R protein. The two sequences are denoted MCP-1RA
CC   and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature
CC   MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB
CC   has a mol. wt. of about 41,000 daltons.
XX
SQ   Sequence 2232 BP; 602 A; 464 C; 508 G; 658 T; 0 other;

  Query Match             49.5%;  Score 980;  DB 16;  Length 2232;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-273;
  Matches  980;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      42 GGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTGTCCACATCTCGTTCT 101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGATTGAACAAGGACGCATTTCCCCAGTACATCCACAACATGCTGTCCACATCTCGTTCT 60

Qy     102 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACCTTTTTTGATTATGAT 161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACCACCTTTTTTGATTATGAT 120

Qy     162 TACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCCTGCCTCCG 221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCCTGCCTCCG 180

Qy     222 CTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCCTCATCTTA 281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCCTCATCTTA 240

Qy     282 ATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 341
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 300

Qy     342 GATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATGAGTGGGTC 401
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATGAGTGGGTC 360

Qy     402 TTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATTTTGGCGGA 461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATTTTGGCGGA 420

Qy     462 ATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATGCTGTGTTT 521
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATGCTGTGTTT 480

Qy     522 GCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCTGGTTGGTG 581
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCTGGTTGGTG 540

Qy     582 GCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAGATTCTGTT 641
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAGATTCTGTT 600

Qy     642 TATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCACACAATAATGAGGAAC 701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAATTTCCACACAATAATGAGGAAC 660

Qy     702 ATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTACTCGGGAATCCTGAAA 761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCTGCTACTCGGGAATCCTGAAA 720

Qy     762 ACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTGAGAGTCATCTTCACC 821
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGGCAGTGAGAGTCATCTTCACC 780

Qy     822 ATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTCATTCTCCTGAACACC 881
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACATTGTCATTCTCCTGAACACC 840

Qy     882 TTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAACTGGACCAAGCCACG 941
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCAGTCAACTGGACCAAGCCACG 900

Qy     942 CAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCCTTC 1001
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     901 CAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCCTTC 960

Qy    1002 GTTGGGGAGAAGTTCAGAAG 1021
           ||||||||||||||||||||
Db     961 GTTGGGGAGAAGTTCAGAAG 980


Search completed: June  1, 2003, 16:20:26
Job time : 1414.56 secs
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